



SEQUENCE LISTING

<110> MA, Jing
GUO, Yajun

<120> PREPARATION AND APPLICATION OF
ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS

<130> 549062000200

<140> US 10/723,003

<141> 2003-11-26

<150> CN 2003101199300

<151> 2003-11-25

<150> CN 031292909

<151> 2003-06-13

<160> 68

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 546

<212> DNA

<213> Homo sapiens

<400> 1

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gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggtggt cctggcacag 240
cgctggatgg agcggctcaa gactgtcgct ggggtccaaga tgcaaggctt gctggagcgc 300
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cgcttcgtcc agaccaacat ctccgcctc ctgcaggaga cctccgagca gctggtggcg 420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
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gccccg                                     546
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<210> 2

<211> 182

<212> PRT

<213> Homo sapiens

<400> 2

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 1             5             10             15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
      20             25             30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
      35             40             45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
      50             55             60
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Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
65					70					75					80
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
				85					90					95	
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
			100					105					110		
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
		115					120					125			
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
	130					135					140				
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
145				150					155						160
Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala
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Thr	Ala	Pro	Thr	Ala	Pro										
				180											

<210> 3
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 3

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ttcgctgtca	aaatccgtga	gctgtctgac	tacctgcttc	aagattacc	agtcaccgtg	180
gctccaacc	tgcaggacga	ggagctctgc	gggggcctct	ggcggctggt	cctggcacag	240
cgctggatgg	agcggctcaa	gactgtcgct	gggtccaaga	tgcaaggctt	gctggagcgc	300
gtgaacacgg	agatacactt	tgtcaccaaa	tgtgcctttc	agccccccc	cagctgtctt	360
cgcttcgtcc	agaccaacat	ctcccgcttc	ctgcaggaga	cctccgagca	gctgggtggc	420
ctgaagccct	ggatcactcg	ccagaacttc	tcccggtgcc	tggagctgca	gtgtcagccc	480
gactcctcaa	ccctgccacc	cccatggagt	ccccggcccc	tggaggccac	agccccgaca	540
gccccggagc	ccaaatcttg	tgacaaaact	cacacatgcc	caccgtgccc	agcacctgaa	600
ctcctggggg	gaccgtcagt	cttcctcttc	cccccaaaac	ccaaggacac	cctcatgata	660
tcccggaacc	ctgaggtcac	atgcgtgggt	gtggacgtga	gccacgaaga	ccctgaggtc	720
aagtccaact	ggtacgtgga	cggcgtggag	gtgcataatg	ccaagacaaa	gccgcgggag	780
gagcagtaca	acagcacgta	ccgggtgggt	tgcgtcctca	ccgtcctgca	ccaggactgg	840
ctgaatggca	aggagtacaa	gtgcaaggtc	tccaacaaag	ccctcccagc	ccccatcgag	900
aaaaccatct	ccaaagccaa	agggcagccc	cgagaaccac	aggtgtacac	cctgccccca	960
tcccgggatg	agctgaccaa	gaaccaggtc	agcctgacct	gcctgggtcaa	aggcttctat	1020
cccagcgaca	tcgccgtgga	gtgggagagc	aatgggcagc	cggagaacaa	ctacaagacc	1080
acgcctcccg	tgctggactc	cgacggctcc	ttcttctct	acagcaagct	caccgtggac	1140
aagagcaggt	ggcagcaggg	gaacgtcttc	tcattgctcc	tgatgcatga	ggctctgcac	1200
aaccactaca	cgcagaagag	cctctccctg	tctcccggtg	aa		1242

<210> 4
 <211> 414
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 4

Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Thr	Thr	Tyr	Leu	Leu	Leu
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Leu	Leu	Leu	Leu	Ser	Ser	Gly	Leu	Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe
			20					25					30		
Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu
		35					40					45			
Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu
	50					55					60				
Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
65					70					75					80
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
				85					90					95	
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
			100					105					110		
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
		115					120					125			
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
	130					135					140				
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
145					150					155					160
Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala
				165					170					175	
Thr	Ala	Pro	Thr	Ala	Pro	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr
			180					185					190		
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe
		195					200					205			
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
	210					215					220				
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
225					230					235					240
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
				245					250					255	
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
			260					265					270		
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
		275					280					285			
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser
	290					295					300				
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
305					310					315					320
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
				325					330					335	
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
			340					345					350		
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
		355					360					365			
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp
	370					375					380				
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
385					390					395					400
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys		
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<210> 5

<211> 45

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 5
 ggcggtggag gctctggtgg aggcggttca ggagcggtg gatct 45

<210> 6
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 6
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 7
 <211> 426
 <212> DNA
 <213> Mus musculus

<400> 7
 atcgccgcca ccatggaatg gagttgata tttctctttc tcctgtcagg aactgcaggt 60
 gtccactctg aggtccagct gcagcagtct ggacctgagc tggtaaagcc tggggcttca 120
 gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg 180
 aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc 240
 actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc 300
 acagcctaca tggagctcag cagactgacc tctgaggact ctgcggtcta ttattgtgtc 360
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 tcctca 426

<210> 8
 <211> 138
 <212> PRT
 <213> Mus musculus

<400> 8
 Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 1 5 10 15
 Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
 50 55 60
 Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
 65 70 75 80
 Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
 85 90 95
 Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
115 120 125
Gly Ala Gly Thr Thr Val Thr Val Ser Ser
130 135

<210> 9
<211> 465
<212> DNA
<213> Mus musculus

<400> 9
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tgtgggaaca ttatgatgac acagtcgcca tcatctctgg ctgtgtctgc aggagaaaag 180
gtcactatga gctgtaagtc cagtcaaagt gttttataca gttcaaata gaagaactac 240
ttggcctggg accagcagaa accagggcag tctcctaaac tgctgatcta ctgggcatcc 300
actaggggaat ctggtgtccc tgatcgcttc acaggcagtg gatctgggac agattttact 360
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<210> 10
<211> 133
<212> PRT
<213> Mus musculus

<400> 10
Met Glu Ser Gln Thr Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
1 5 10 15
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20 25 30
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
35 40 45
Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
85 90 95
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
100 105 110
Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys
115 120 125
Leu Glu Ile Lys Arg
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<210> 11
<211> 2021
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 11
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aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc 240
actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc 300
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tctgggggca cagcggccct gggtgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtga caagaaagtt 720
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gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
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<210> 12

<211> 468

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 12

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Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1           5           10           15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
20           25           30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35           40           45
Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
50           55           60
Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65           70           75           80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
85           90           95
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
100          105          110

```

Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
 115 120 125
 Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 130 135 140
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 145 150 155 160
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 165 170 175
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 180 185 190
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 195 200 205
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 210 215 220
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
 225 230 235 240
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 245 250 255
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 260 265 270
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285
 His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
 290 295 300
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 305 310 315 320
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 325 330 335
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 340 345 350
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 355 360 365
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 370 375 380
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460
 Ser Pro Gly Lys
 465

<210> 13

<211> 786

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 13

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tgtgggaaca ttatgatgac acagtcgcca tcattctctg ctgtgtctgc aggagaaaag 180
gtcactatga gctgtaagtc cagtcaaagt gttttatata gttcaaata caagaactac 240
ttggcctggg accagcagaa accagggcag tctcctaaac tgctgatcta ctgggcatcc 300
actaggggaat ctggtgtccc tgatcgcttc acaggcagtg gatctgggac agattttact 360
cttaccatca gcagtgtaca agctgaagac ctggcagttt attactgtca tcaatatttc 420
tcctcataca cgttcggagg ggggaccaag ctggaaataa agcggactgt ggctgcacca 480
tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttggt 540
tgctgtctga ataacttcta tcccagagag gccaaagtac agtggaagggt ggataacgcc 600
ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 660
agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 720
tgcgaaagtca cccatcaggg cctgagctcg cccgtcacia agagcttcaa caggggagag 780
tggttag

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<210> 14

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 14

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Met Glu Ser Gln Thr Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
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Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
          20          25          30
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
          35          40          45
Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
          50          55          60
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65          70          75          80
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
          85          90          95
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
          100          105          110
Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys
          115          120          125
Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
          130          135          140
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145          150          155          160
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
          165          170          175
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
          180          185          190
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
          195          200          205
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210          215          220
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225          230          235

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<210> 15

<211> 426
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 15
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 ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtgat gacatgggtg 180
 cgccaagccc ccggaaggc cctcgaatgg attggctaca ttgtgcctta taatgacggt 240
 actaagtaca atgaaaagtt caagggcaga ttacaatat caagtgacaa gagcaagtca 300
 accgcattcc tccaaatgga cagcttgctg ccagaggaca ccgccgtata ctattgtgtg 360
 cgcggcagcc gttacgactg gtacttggac tactggggcc aaggcactcc agtcaccgctc 420
 tcctct 426

<210> 16
 <211> 138
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 16
 Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
 1 5 10 15
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
 20 25 30
 Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
 65 70 75 80
 Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
 85 90 95
 Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
 115 120 125
 Gly Gln Gly Thr Pro Val Thr Val Ser Ser
 130 135

<210> 17
 <211> 465
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 17
 gagcattacc ggccatactc atcaccatcc caggatatct ctagaaagct tgccgccacc 60
 atggattttc aagtgcagat ttccagcttc ctgctaataca gtgcttcagt cataatgtcc 120

```

agaggaaaca tcattgatgac tcagagccca tccagcttga gcgcatcagt aggcgaccgc 180
gtaacgatca cttgcaaata ctctcagtca gtattgtact ccagcaacca gaagaactac 240
ctggccggat atcagcagac tcccggcaaa gcccacaaagt tgctgattta ttgggcctcc 300
acgcgcgagt ctggcgtgcc atcacgcttt agcggcagcg ggtccggtac agattacacg 360
tttaccatta gcagtctgca gcctgaggac atagccacct actactgtca ccagtacttt 420
agttcctaca cttttggcca gggaactaaa ctgcagatta ctgca 465

```

<210> 18

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 18

```

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1          5          10          15
Val Ile Met Ser Arg Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser
20          25          30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser
35          40          45
Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
50          55          60
Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser
65          70          75          80
Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
85          90          95
Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
100          105          110
Thr Tyr Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gln Gly
115          120          125
Thr Lys Leu Gln Ile Thr Arg
130          135

```

<210> 19

<211> 2021

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 19

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agagccgcca ccatggattg ggtgtggacc ttgctattcc tgttgtcagt aactgcaggt 60
gtccactccc aggtgcagct ggtgcagtct ggcggtggag tgggccagcc cggccgcagc 120
ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtgat gacatgggtg 180
cgccaagccc ccggaaggc cctcgaatgg attggctaca ttgtgcctta taatgacggc 240
actaagtaca atgaaaagtt caagggcaga ttacaatat caagtgacaa gagcaagtca 300
accgcattcc tccaaatgga cagcttgctg ccagaggaca ccgccgtata ctattgtgtg 360
cgcggcagcc gttacgactg gtacttgga cactggggcc aaggcactcc agtcaccgtc 420
tcctctgcta gcaccaaggg cccatcggtc tccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcggtgcaca ccttccccgc tgtcctacag 600
tctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag ccagcaaca ccaaggtgga caagaaagtt 720

```

```

ggtgagagggc cagcacaggg agggaggggtg tctgctggaa gcaggctcag cgctcctgcc 780
tggacgcatac ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
ttcacccgga gcctctgccc gccccactca tgctcagggg gaggggtcttc tggctttttc 900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccac ggccctgcac acaaagggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gacctgccc ctgacctaaag 1020
cccccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat 1080
tccagtaact cccaatcttc tctctgcaga gcccaaactt tgtgacaaaa ctcacacatg 1140
cccaccgtgc ccaggtaagc cagcccaggc ctgcgccctc agctcaaggc gggacagggtg 1200
ccctagagta gcctgcatcc agggacaggc ccagccggg tgctgacacg tccacctcca 1260
tctcttcttc agcacctgaa ctccctggggg gaccgtcagt ctctctcttc ccccaaaac 1320
ccaaggacac cctcatgate tcccggaccc ctgaggtcac atgcgtgggtg gtggacgtga 1380
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ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtgggtc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc tccaacaaaag 1560
ccctcccagc ccccatcgag aaaacctatc ccaaagccaa aggtgggacc cgtgggggtgc 1620
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gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctcccgctgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaatg a 2021

```

<210> 20

<211> 468

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 20

```

Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
1          5          10          15
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
20          25          30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35          40          45
Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50          55          60
Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65          70          75          80
Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
85          90          95
Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
100          105          110
Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
115          120          125
Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130          135          140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145          150          155          160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
165          170          175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
180          185          190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr

```

195	200	205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn		
210	215	220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser		
225	230	235
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu		
245	250	255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu		
260	265	270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser		
275	280	285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu		
290	295	300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr		
305	310	315
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn		
325	330	335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro		
340	345	350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln		
355	360	365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val		
370	375	380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val		
385	390	395
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro		
405	410	415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr		
420	425	430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val		
435	440	445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu		
450	455	460
Ser Pro Gly Lys		
465		

<210> 21

<211> 786

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 21

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agaggaaaca	tcattgatgac	tcagagccca	tccagcttga	gcgcattcagt	aggcgaccgc	180
gtaacgatca	cttgcaaatc	ctctcagtca	gtattgtact	ccagcaacca	gaagaactac	240
ctggccggat	atcagcagac	tcccggcaaa	gccccaaagt	tgctgattta	ttgggcctcc	300
acgcgcgagt	ctggcgtgcc	atcacgcttt	agcggcagcg	ggtccgggtac	agattacacg	360
tttaccatta	gcagtctgca	gcctgaggac	atagccacct	actactgtca	ccagtacttt	420
agttcctaca	cttttgccca	gggaactaaa	ctgcagatta	ctcgaactgt	ggctgcacca	480
tctgtcttca	tcttcccgcc	atctgatgag	cagttgaaat	ctggaactgc	ctctgtttgtg	540
tgcctgctga	ataacttcta	tcccagagag	gccaaagtac	agtggaaggt	ggataacgcc	600
ctccaatcgg	gtaactccca	ggagagtgtc	acagagcagg	acagcaagga	cagcacctac	660

```

agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 720
tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag 780
tgtagtag                                     786

```

```

<210> 22
<211> 241
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic Construct

```

```

<400> 22
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1           5           10           15
Val Ile Met Ser Arg Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser
      20           25           30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser
      35           40           45
Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
      50           55           60
Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser
65           70           75           80
Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
      85           90           95
Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
      100          105          110
Thr Tyr Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gln Gly
      115          120          125
Thr Lys Leu Gln Ile Thr Arg Thr Val Ala Ala Pro Ser Val Phe Ile
      130          135          140
Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
145          150          155          160
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
      165          170          175
Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
      180          185          190
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
      195          200          205
Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
      210          215          220
His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
225          230          235          240
Cys

```

```

<210> 23
<211> 2489
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Synthetic Construct

```

```

<400> 23
agagccgcca ccatggattg ggtgtggacc ttgctattcc tggtgtcagt aactgcaggt 60

```

```

gtccactccc aggtgcagct ggtgcagctt ggcgggtggag tgggtccagcc cggccgcagc 120
ctgagggtgt cctgcaaggc atctggctac accttcacca gctacgtgat gacatgggtg 180
cgccaagccc ccggaaggc cctcgaatgg attggctaca ttgtgcctta taatgacggg 240
actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtca 300
accgcattcc tccaaatgga cagcttgctg ccagaggaca ccgccgtata ctattgtgtg 360
cggggcagcc gttacgactg gtacttggtg tactggggcc aaggcactcc agtcaccgtc 420
tcctctgcta gcaccaaggg cccatcggtc ttccccctgg caccctcttc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accgggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag ccagcaaca ccaagggtgga caagaaagt 720
ggtgagaggc cagcacaggg agggaggggtg tctgttgga gcaggctcag cgctcctgcc 780
tggacgcata ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
ttcaccggga gctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc 900
ccaggctctg ggcaggcaca ggctagggtgc ccctaaccga ggccctgcac acaaaggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaa 1020
cccaccccaa aggccaaact ctccactccc tcagctcgga cactttctct cctcccagat 1080
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ccaaggacac cctcatgatc tcccggacc ctgaggtcac atgcgtgggtg gtggacgtga 1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
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ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag 1560
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cctccgagca gctgggtggc ctgaagccct ggatcactcg ccagaacttc tcccgggtgcc 2400
tggagctgca gtgtcagccc gactcctcaa ccctgccacc ccatggagt ccccggtccc 2460
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2489

```

<210> 24

<211> 624

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 24

```

Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
 1           5           10          15
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
          20          25          30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35          40          45

```

Thr	Ser	Tyr	Val	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
50						55					60				
Glu	Trp	Ile	Gly	Tyr	Ile	Val	Pro	Tyr	Asn	Asp	Gly	Thr	Lys	Tyr	Asn
65					70					75					80
Glu	Lys	Phe	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ser	Asp	Lys	Ser	Lys	Ser
				85					90					95	
Thr	Ala	Phe	Leu	Gln	Met	Asp	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val
			100					105					110		
Tyr	Tyr	Cys	Ala	Arg	Gly	Ser	Arg	Tyr	Asp	Trp	Tyr	Leu	Asp	Tyr	Trp
		115					120					125			
Gly	Gln	Gly	Thr	Pro	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro
	130					135					140				
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
145					150					155					160
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
				165					170					175	
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
			180					185					190		
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
		195					200					205			
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
	210					215					220				
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
225					230					235					240
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
				245					250					255	
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
			260					265					270		
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
		275					280					285			
His	Glu	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Asp	Gly	Val	Glu
	290					295					300				
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
305					310					315					320
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
				325					330					335	
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro
			340					345					350		
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
		355					360					365			
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val
	370					375					380				
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val
385					390					395					400
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro
				405					410					415	
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	
			420					425					430		
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val
		435					440					445			
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu
	450					455					460				
Ser	Pro	Gly	Lys	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser
465					470					475					480
Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln
				485					490					495	
Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys


```

ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
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```

<210> 26

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 26

```

Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
 1          5          10          15
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
          20          25          30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe

          35          40          45
Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
          50          55          60
Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65          70          75          80
Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
          85          90          95
Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
          100          105          110
Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
          115          120          125
Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
          130          135          140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145          150          155          160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
          165          170          175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
          180          185          190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
          195          200          205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
          210          215          220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225          230          235          240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
          245          250          255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
          260          265          270

```

Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser		
		275					280					285					
His	Glu	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Asp	Gly	Val	Glu		
	290					295					300						
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr		
305					310					315					320		
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn		
				325					330					335			
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro		
		340						345					350				
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln		
	355					360						365					
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val		
	370					375					380						
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val		
385				390						395					400		
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro		
				405					410					415			
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr		
			420					425					430				
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val		
	435					440					445						
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu		
	450					455					460						
Ser	Pro	Gly	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly		
465				470						475					480		
Gly	Gly	Ser	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser		
				485					490					495			
Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp		
			500					505					510				
Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly		
	515						520					525					
Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys		
	530					535					540						
Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr		
545				550						555					560		
Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys		
				565				570						575			
Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser		
			580					585					590				
Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser		
	595					600						605					
Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Pro	Pro		
	610				615						620						
Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala	Thr	Ala	Pro	Thr	Ala	Pro			
625					630					635							

<210> 27

<211> 1986

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 27

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ttcgtgtgca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggtggtt cctggcacag 240
cgctggatgg agcgggtcaa gactgtcgct ggggtccaaga tgcaaggctt gctggagcgc 300
gtgaacacgg agatacactt tgtcaccaa tgtgcctttc agcccccccc cagctgtctt 360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctgggtggc 420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca 540
gccccggagc ccaaactctg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 600
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 660
tcccggacc ctaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 720
aagttcaact ggtactgtga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg 840
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aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 960
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tccggtacag attacacggt taccattagc agcttgcagc ctgaggacat agccacctac 1920
tactgtcacc agtactttag ttctacact tttggccagg gaactaaact gcagattact 1980
cgatga

```

<210> 28

<211> 661

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 28

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Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1          5          10          15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
 20          25          30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
 35          40          45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50          55          60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 65          70          75          80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 85          90          95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala

```


Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ser	Ser	Gln	Ser
				565					570					575	
Val	Leu	Tyr	Ser	Ser	Asn	Gln	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln
			580					585					590		
Thr	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg
		595					600					605			
Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
	610					615					620				
Tyr	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr
625					630				635						640
Tyr	Cys	His	Gln	Tyr	Phe	Ser	Ser	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys
			645					650						655	
Leu	Gln	Ile	Thr	Arg											
			660												

<210> 29

<211> 2489

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 29

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gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg 180
aagcagaagc ctggggcaggg ccttgactgg attggatata ttgttcctta caatgatggc 240
actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc 300
acagcctaca tggagctcag cagactgacc tctgaggact ctgcggtcta ttattgtgtc 360
tacggtagta ggtacgactg gtatttagat gtctggggcg cagggaccac ggtcacctgc 420
tcctcagcta gcaccaaggg cccatcggtc tccccctgg caccctcctc caagagcacc 480
tctgggggca cagcgccctt gggctgctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttccccgc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtga caagaaagtt 720
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ttcacccgga gcctctgccc gccccactca tgctcaggga gagggctctc tggctttttc 900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccga ggccctgcac acaaaggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaaag 1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat 1080
tccagtaact cccaatcttc tctctgcaga gcccaaactt tgtgacaaaa ctcacacatg 1140
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gccacgaaga ccttgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtgggtc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggct tccaacaaag 1560
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gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta 1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg ccccatccc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920

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gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaaac ccaggactgc tccttccaac 2040
acagcccatc ctccctccgac ttcgctgtca aaatccgtga gctgtctgac tacctgcttc 2100
aagattaccc agtcaccgtg gcctccaacc tgcaggacga ggagctctgc gggggcctct 2160
ggcggctggt cctggcacag cgctggatgg agcggctcaa gactgtcgct ggggtccaaga 2220
tgcaaggctt gctggagcgc gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc 2280
agcccccccc cagctgtctt cgcttcgtcc agaccaacat ctcccgcttc ctgcaggaga 2340
cctccgagca gctggtggcg ctgaagccct ggatcactcg ccagaacttc tcccggtgcc 2400
tggagctgca gtgtcagccc gactcctcaa ccctgccacc cccatggagt ccccggtccc 2460
tggaggccac agccccgaca gcccgtga                                     2489

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<210> 30

<211> 624

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 30

```

Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 1           5           10           15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
          20          25          30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
          35          40          45
Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
          50          55          60
Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65          70          75          80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
          85          90          95
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
          100         105         110
Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
          115         120         125
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
          130         135         140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145         150         155         160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
          165         170         175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
          180         185         190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
          195         200         205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
          210         215         220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225         230         235         240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
          245         250         255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
          260         265         270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
          275         280         285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu

```

290		295		300
Val His Asn Ala Lys Thr	Lys Pro Arg Glu Glu	Gln Tyr Asn Ser Thr		
305		310		315
Tyr Arg Val Val Ser Val	Leu Thr Val Leu His	Gln Asp Trp Leu Asn		320
		325		330
Gly Lys Glu Tyr Lys Cys	Lys Val Ser Asn Lys	Ala Leu Pro Ala Pro		335
		340		345
Ile Glu Lys Thr Ile Ser	Lys Ala Lys Gly Gln	Pro Arg Glu Pro Gln		350
		355		360
Val Tyr Thr Leu Pro Pro	Ser Arg Asp Glu Leu	Thr Lys Asn Gln Val		365
		370		375
Ser Leu Thr Cys Leu Val	Lys Gly Phe Tyr Pro	Ser Asp Ile Ala Val		380
385		390		395
Glu Trp Glu Ser Asn Gly	Gln Pro Glu Asn Asn	Tyr Lys Thr Thr Pro		400
		405		410
Pro Val Leu Asp Ser Asp	Gly Ser Phe Phe Leu	Tyr Ser Lys Leu Thr		415
		420		425
Val Asp Lys Ser Arg Trp	Gln Gln Gly Asn Val	Phe Ser Cys Ser Val		430
		435		440
Met His Glu Ala Leu His	Asn His Tyr Thr Gln	Lys Ser Leu Ser Leu		445
		450		455
Ser Pro Gly Lys Thr Gln	Asp Cys Ser Phe Gln	His Ser Pro Ile Ser		460
465		470		475
Ser Asp Phe Ala Val Lys	Ile Arg Glu Leu Ser	Asp Tyr Leu Leu Gln		480
		485		490
Asp Tyr Pro Val Thr Val	Ala Ser Asn Leu Gln	Asp Glu Glu Leu Cys		495
		500		505
Gly Gly Leu Trp Arg Leu	Val Leu Ala Gln Arg	Trp Met Glu Arg Leu		510
		515		520
Lys Thr Val Ala Gly Ser	Lys Met Gln Gly Leu	Leu Glu Arg Val Asn		525
		530		535
Thr Glu Ile His Phe Val	Thr Lys Cys Ala Phe	Gln Pro Pro Pro Ser		540
545		550		555
Cys Leu Arg Phe Val Gln	Thr Asn Ile Ser Arg	Leu Leu Gln Glu Thr		560
		565		570
Ser Glu Gln Leu Val Ala	Leu Lys Pro Trp Ile	Thr Arg Gln Asn Phe		575
		580		585
Ser Arg Cys Leu Glu Leu	Gln Cys Gln Pro Asp	Ser Ser Thr Leu Pro		590
		595		600
Pro Pro Trp Ser Pro Arg	Pro Leu Glu Ala Thr	Ala Pro Thr Ala Pro		605
		610		615
				620

<210> 31

<211> 2534

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 31

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gtccactctg aggtccagct gcagcagctt ggacctgagc tggtaaagcc tggggcttca 120
gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg 180
aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc 240
actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc 300

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```

acagcctaca tggagctcag cagactgacc tctgaggact ctgcggtcta ttattgtgtc 360
tacggtagta ggtacgactg gtatttagat gtctggggcg cagggaccac ggtcaccgtc 420
tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 480
tctgggggca cagcggccct gggctgacct gtcaaggact acttccccga accggtgacg 540
gtgtcttga actcaggcgc cctgaccagc ggcgtgcaca ccttccccgc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
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tctcttctc agcâcctgââ ctctggggg gâcctcâgt cttctcttc cccâââââc 1320
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gccâcâgââ ccctgâggtc ââgttcaâct ggtâcgtgââ cggcgtggâg gtgcââââtg 1440
câââgââââ gccgcgggâg gâgcâgtâcâ âcâgcâcgtâ ccgggtggct tgcgtcctcâ 1500
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ctccâgtgct ggâctccgâc ggctccttct tctctâcâg cââgtcâc gtggâcâââ 1920
gcâggtggââ gcâgggâââc gtcttctcâ gtctcgtgâ gcâtgâggt ctgcââââc 1980
âctâcâcgcâ gâââgâcctc tccctgtctc ccggtââââg cgggtggâggc tctgggtggâg 2040
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tggcgtgâââ gccctggâtc âctcâccâgâ âcttctccâg gtgctggâg ctgâcâgtg 2460
âgcccâgâct ctcââcctg ccâccccâct ggâgtccccg gccctggâg gccâcâgccc 2520
cgâcâgcccc gtgâ 2534

```

<210> 32
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 32
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 1 5 10 15
 Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
 50 55 60
 Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn

65					70					75					80
Glu	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ser	Asp	Lys	Ser	Ser	Ser
				85					90					95	
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Arg	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
			100					105					110		
Tyr	Tyr	Cys	Val	Tyr	Gly	Ser	Arg	Tyr	Asp	Trp	Tyr	Leu	Asp	Val	Trp
		115					120					125			
Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro
	130						135				140				
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
145					150					155					160
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
			165						170					175	
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
			180					185					190		
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
		195					200					205			
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
	210					215						220			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
225				230						235					240
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
			245						250					255	
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
		260						265					270		
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
		275					280						285		
His	Glu	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Asp	Gly	Val	Glu
	290					295					300				
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
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Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
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Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro
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Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
		355					360					365			
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val
	370					375					380				
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Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro
			405						410					415	
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr
			420					425					430		
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val
		435					440					445			
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	450					455					460				
Ser	Pro	Gly	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
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Gly	Gly	Ser	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser
			485						490					495	
Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp
		500						505					510		
Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly
		515					520					525			

Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys
530						535					540				
Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr
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Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys
				565					570					575	
Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser
			580					585				590			
Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser
		595					600					605			
Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Pro	Pro
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<210> 33

<211> 1986

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 33

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gcctccaacc	tgcaggacga	ggagctctgc	gggggcctct	ggcggctggt	cctggcacag	240
cgctggatgg	agcgggtcaa	gactgtcgct	gggtccaaga	tgcaaggctt	gctggagcgc	300
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cgcttcgtcc	agaccaacat	ctcccgcctc	ctgcaggaga	cctccgagca	gctgggtggc	420
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gactcctcaa	ccctgccacc	cccatggagt	ccccggcccc	tggaggccac	agccccgaca	540
gccccggagc	ccaaatcttg	tgacaaaact	cacacatgcc	caccgtgccc	agcacctgaa	600
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tcccggaccc	ctgaggtcac	atgcgtgggt	gtggacgtga	gccacgaaga	ccctgaggtc	720
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cccagcgaca	tcgccgtgga	gtgggagagc	aatgggcagc	cggagaacaa	ctacaagacc	1080
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tcaaatacaga	agaactactt	ggcctgggtac	cagcagaaac	cagggcagtc	tcctaaactg	1800
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tctgggacag	attttactct	taccatcagc	agtgtacaag	ctgaagacct	ggcagtttat	1920

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 355 360 365
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 370 375 380
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 385 390 395 400
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Glu Val

 405 410 415
 Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val
 420 425 430
 Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Val Met
 435 440 445
 His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Asp Trp Ile Gly Tyr
 450 455 460
 Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly
 465 470 475 480
 Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu
 485 490 495
 Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Tyr
 500 505 510
 Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp Gly Ala Gly Thr Thr
 515 520 525
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 530 535 540
 Gly Gly Gly Ser Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
 545 550 555 560
 Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
 565 570 575
 Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
 580 585 590
 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 595 600 605
 Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
 610 615 620
 Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
 625 630 635 640
 Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys
 645 650 655
 Leu Glu Ile Lys Arg
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<210> 35

<211> 426

<212> DNA

<213> Mus musculus

<400> 35

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 atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag 180
 acacctggtc ggggcctgga atggattgga gctattttatc caggaaatgg tgatacttcc 240
 tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcc 300
 tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg 360
 acttactacg gcggtgactg gtacttcaat gtctggggcg cagggaccac ggtcaccgctc 420
 tctgca 426

<210> 36
 <211> 140
 <212> PRT
 <213> Mus musculus

<400> 36
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 1 5 10 15
 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
 50 55 60
 Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
 65 70 75 80
 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
 115 120 125
 Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala
 130 135 140

<210> 37
 <211> 390
 <212> DNA
 <213> Mus musculus

<400> 37
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 aaggtcacaa tgacttgtag ggccagctca agtgtaagtt acatccactg gttccagcag 180
 aagccaggat cctcccccaa accctggatt tatgccacat ccaacctggc ttctggagtc 240
 cctgttcgct tcagtggcag tgggtctggg acctcttact ctctcacaat cagtagagtg 300
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 ggtggtggga ccaagctgga gatcaaacga 390

<210> 38
 <211> 129
 <212> PRT
 <213> Mus musculus

<400> 38
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 1 5 10 15
 Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80

Val	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
			85						90				95		
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
		100					105					110			
Thr	Ser	Asn	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys
		115					120					125			

Arg

<210> 39

<211> 2021

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 39

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atgtcctgca aggcttctgg ctacacattt accagttaca atatgcaact ggtaaagcag 180
acacctggtc ggggcctgga atggattgga gctatttatc caggaaatgg tgatacttcc 240
tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcc 300
tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg 360
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tctgcagcta gcaccaaggg cccatcggtc tccccctgg caccctctc caagagcacc 480
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cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtga caagaaagtt 720
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gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tcctgtctc cgggtaaatg a 2021

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<210> 40

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 40

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Val	His	Ser	Gln	Val	Gln	Leu	Gln	Gln	Pro	Gly	Ala	Glu	Leu	Val	Lys
			20					25					30		
Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
		35					40					45			
Thr	Ser	Tyr	Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Gly	Arg	Gly	Leu
	50					55					60				
Glu	Trp	Ile	Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn
65					70				75						80
Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser
				85					90					95	
Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
			100					105					110		
Tyr	Tyr	Cys	Ala	Arg	Ser	Thr	Tyr	Tyr	Gly	Gly	Asp	Trp	Tyr	Phe	Asn
		115					120					125			
Val	Trp	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ala	Ala	Ser	Thr	Lys
	130					135					140				
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly
145					150					155					160
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro
				165					170					175	
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr
			180					185					190		
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val
		195					200					205			
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn
	210					215						220			
Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro
225					230					235					240
Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu
				245					250					255	
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp
			260					265					270		
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
	275						280					285			
Val	Ser	His	Glu	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Asp	Gly
	290					295					300				
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn
305					310					315					320
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp
				325					330					335	
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro
		340						345					350		
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu
		355					360					365			
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn
	370					375					380				
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile
385					390					395					400
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr

				405					410					415			
Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys		
			420					425					430				
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys		
		435					440					445					
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu		
	450					455					460						
Ser	Leu	Ser	Pro	Gly	Lys												
465					470												

<210> 41

<211> 711

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 41

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aaggtcacia tgacttgca ggccagctca agtgtaagtt acatccactg gttccagcag 180
aagccaggat cctcccccaa accctggatt tatgccacat ccaacctggc ttctggagtc 240
cctgttcgct tcagtggcag tgggtctggg acctcttact ctctcacaat cagtagagtg 300
gaggctgaag atgctgccac ttattactgc cagcagtgga ctagtaacct acccacgttc 360

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gggtggtggga ccaagctgga gatcaaacga actgtggctg caccatctgt cttcatcttc 420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac 540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600
ctgacgctga gcaaagcaga ctacgagaaa cacaagtct acgcctgcga agtcacccat 660
cagggcctga gctcgcccgt cacaagagc ttcaacaggg gagagtgtta g 711

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<210> 42

<211> 235

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 42

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser		
1				5				10					15				
Val	Ile	Met	Ser	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile		
			20					25					30				
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser		
		35					40					45					
Ser	Ser	Val	Ser	Tyr	Ile	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Ser	Ser		
	50					55					60						
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro		
65				70						75				80			
Val	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile		
			85					90					95				
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp		


```

ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg ccccatccc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctccccgtgt ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaaac ccaggactgc tccttccaac 2040
acagcccatc ctctccgac ttcgctgtca aaatccgtga gctgtctgac tacctgcttc 2100
aagattaccc agtcaccgtg gcctccaacc tgcaggacga ggagctctgc gggggcctct 2160
ggcggctggg cctggcacag cgctggatgg agcggctcaa gactgtcgct ggggtccaaga 2220
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cctccgagca gctgggtggc ctgaagccct ggatcactcg ccagaacttc tcccggtgcc 2400
tgagctgca gtgtcagccc gactcctcaa ccctgccacc cccatggagt ccccggtccc 2460
tgaggccac agccccgaca gccccgtga 2489

```

<210> 44

<211> 626

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 44

```

Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
 1           5           10           15
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
      20           25           30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
      35           40           45
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
      50           55           60
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
65           70           75           80
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
      85           90           95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
      100          105          110
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
      115          120          125
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys
      130          135          140
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145          150          155          160
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
      165          170          175
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
      180          185          190
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
      195          200          205
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
      210          215          220
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225          230          235          240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
      245          250          255
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp

```


<400> 45

```
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tcccaggtac aactacagca gcctggggct gagctgggtga agcctggggc ctcagtgaag 120
atgtcctgca aggcttctgg ctacacattt accagttaca atatgactg ggtaaagcag 180
acacctggtc ggggcctgga atggattgga gctattttatc caggaaatgg tgatacttcc 240
tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcc 300
tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg 360
acttactacg gcggtgactg gtacttcaat gtctggggcg cagggaccac ggtcaccgtc 420
tctgcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagt 720
ggtgagaggg cagcacaggg agggaggggtg tctgctggaa gcaggctcag cgctcctgcc 780
tgagcgcac ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
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ccaggctctg ggcaggcaca ggctaggtgc ccctaacca ggcctgcac acaaaggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaa 1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat 1080
tccagtaact cccaatcttc tctctgcaga gcccaaact tgtgacaaaa ctcacacatg 1140
cccaccgtgc ccaggtaaag cagcccaggc ctgcacctcc agctcaaggc gggacagggtg 1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
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gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag 1560
ccctcccaga ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtgggggtg 1620
gagggccaca tggacagagg ccggctcgcc ccacctctg ccctgagagt gaccgtgta 1680
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gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctcccgtgct ggactccgac ggctcttct tctctacag caagctcacc gtggacaaga 1920
gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaagg cgggtggagg tctgggtggag 2040
gcggttcagg aggcgggtgga tctaccagg actgtcctt ccaacacagc cccatctcct 2100
ccgacttcgc tgtcaaaatc cgtgagctgt ctgactacct gcttcaagat taccagtc 2160
ccgtggcctc caacctgcag gacgaggagc tctgcggggg cctctggcgg ctggtcctgg 2220
cacagcgtg gatggagcgg ctcaagactg tcgctgggtc caagatgcaa ggcttgctgg 2280
agcgcgtgaa cacggagata cactttgtca ccaaagtgtc ctttcagccc cccccagct 2340
gtcttcgctt cgtccagacc aacatctccc gcctcctgca ggagacctcc gagcagctgg 2400
tggcgctgaa gccctggatc actcgccaga acttctcccg gtgcctggag ctgcagtgtc 2460
agcccgactc ctcaaccctg ccacccccat ggagtccccg gccctggag gccacagccc 2520
cgacagcccc gtga 2534
```

<210> 46

<211> 641

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 46

```
Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
1           5           10           15
```


Ser	Leu	Ser	Pro	Gly	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	465
					470					475						480
Gly	Gly	Gly	Gly	Ser	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	
				485					490						495	
Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	
			500					505					510			
Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	
	515					520						525				
Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	
	530					535					540					
Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	
545					550				555						560	
Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	
				565					570					575		
Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	
			580					585					590			
Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	
		595					600					605				
Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	
	610					615					620					
Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala	Thr	Ala	Pro	Thr	Ala	
625					630					635					640	
Pro																

<210> 47

<211> 1974

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 47

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agctcgggac	tcagtgggac	ccaggactgc	tccttccaac	acagcccat	ctcctccgac	120
ttcgtgtgca	aaatccgtga	gctgtctgac	tacctgcttc	aagattaccc	agtcaccgtg	180
gcctccaacc	tgcaggacga	ggagctctgc	gggggcctct	ggcggctggg	cctggcacag	240
cgctggatgg	agcggctcaa	gactgtcgct	gggtccaaga	tgcaaggctt	gctggagcgc	300
gtgaacacgg	agatacactt	tgtaacacaa	tgtgcctttc	agccccccc	cagctgtctt	360
cgcttcgtcc	agaccaacat	ctcccgcctc	ctgcaggaga	cctccgagca	gctgggtggc	420
ctgaagccct	ggatcactcg	ccagaacttc	tcccggtgcc	tggagctgca	gtgtcagccc	480
gactcctcaa	cctgccacc	cccatggagt	ccccggcccc	tggaggccac	agccccgaca	540
gccccggagc	ccaaatcttg	tgacaaaact	cacacatgcc	caccgtgccc	agcacctgaa	600
ctcctggggg	gaccgtcagt	cttcctcttc	ccccaaaac	ccaaggacac	cctcatgac	660
tcccggaccc	ctgaggtcac	atgcgtgggtg	gtggacgtga	gccacgaaga	ccctgaggtc	720
aagttcaact	ggtacgtgga	cggcgtggag	gtgcataatg	ccaagacaaa	gccgcgggag	780
gagcagtaca	acagcacgta	ccgggtgggtc	tgcgtcctca	ccgtcctgca	ccaggactgg	840
ctgaatggca	aggagtacaa	gtgcaaggctc	tccaacaaag	ccctcccagc	ccccatcgag	900
aaaaccatct	ccaaagccaa	agggcagccc	cgagaaccac	aggtgtacac	cctgccccca	960
tcccgggatg	agctgaccaa	gaaccaggctc	agcctgacct	gctgggtcaa	aggcttctat	1020
cccagcgaca	tcgccgtgga	gtgggagagc	aatgggcagc	cggagaacaa	ctacaagacc	1080
acgcctccc	tgtgtgactc	cgacggctcc	ttcttctct	acagcaagct	caccgtggac	1140
aagagcaggt	ggcagcagg	gaacgtcttc	tcatgctccg	tgatgcatga	ggctctgcac	1200
aaccactaca	cgcagaagag	cctctccctg	tctcccggtg	aacaggtaca	actacagcag	1260
cctggggctg	agctggtgaa	gcctggggcc	tcagtgaaga	tgtcctgcaa	ggcttctggc	1320

```

tacacattta ccagttacaa tatgcactgg gtaaagcaga cacctggtcg gggcctggaa 1380
tggtattggag ctatttatcc aggaaatggt gatacttcct acaatcagaa gttcaagggc 1440
aaggccacac tgactgcaga caaatcctcc agcacagcct acatgcagct cagcagcctg 1500
acatctgaag actctgcggg ctattactgt gcaagatcga cttactacgg cgggtgactgg 1560
tacttcaatg tctggggcgc agggaccacg gtcaccgtct ctgcaggcgg tggaggctct 1620
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ctgtctgcat ctccagggga gaaggtcaca atgacttgca gggccagctc aagtgttaagt 1740
tacatccact ggttcagca gaagccagga tcctcccca aaccctggat ttatgccaca 1800
tccaacctgg cttctggagt ccctgttcgc ttcagtggca gtgggtctgg gacctcttac 1860
tctctcacia tcagtagagt ggaggctgaa gatgctgcca cttattactg ccagcagtgg 1920
actagtaacc caccacggt cggtgggtgg accaagctgg agatcaaacy atga 1974

```

<210> 48

<211> 657

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 48

```

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1          5          10          15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
20          25          30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
35          40          45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50          55          60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65          70          75          80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
85          90          95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
100         105         110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
115         120         125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
130         135         140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145         150         155         160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
165         170         175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
180         185         190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
195         200         205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
210         215         220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225         230         235         240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
245         250         255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
260         265         270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
275         280         285

```



```

<400> 49
atggattttc aggtgcagat tttcagcttc ctgctaataca gtgcctcagt cataatatcc 60
agaggagagg ttcagctggg ggagtctggc ggtggcctgg tgcagccagg gggctcactc 120
cgtttgcctt gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt 180
caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact 240
agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca 300
gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga 360
tggggagggg acggcttcta tgctatggac tactgggggc aaggaaccct ggtcaccgtc 420
tcctcg
426

```

```

<210> 50
<211> 142
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic Construct

```

```

<400> 50
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1           5           10          15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
20          25          30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35          40          45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
50          55          60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
65          70          75          80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
85          90          95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
100         105         110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
115         120         125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130         135         140

```

```

<210> 51
<211> 390
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Synthetic Construct

```

```

<400> 51
atggattttc aggtgcagat tttcagcttc ctgctaataca gtgcctcagt cataatatcc 60
agaggagaca tccagatgac ccagtcctcg agtcctctgt ccgcctctgt gggcgatagg 120
gttaccatca cctgccgtgc cagtcaggat gtgaatactg ctgtagcctg gtatcaacag 180
aaaccaggaa aagctccgaa actactgatt tactcggcat ccttctctta ctctggagtc 240
ccttctcgct tctctggctc cagatctggg acggatttca ctctgacctg cagcagctctg 300
cagccggaag acttcgcaac ttattactgt cagcaacatt atactactcc tcccacgttc 360
ggacagggta ccaaggtgga gatcaaactg
390

```

<210> 52
 <211> 130
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 52
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 20 25 30
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 35 40 45
 Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50 55 60
 Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val
 65 70 75 80
 Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr
 85 90 95
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 115 120 125
 Lys Arg
 130

<210> 53
 <211> 2021
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 53
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 agaggagagg ttcagctggg ggagctctggc ggtggcctgg tgcagccagg gggctcactc 120
 cgtttgtcct gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt 180
 caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact 240
 agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca 300
 gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga 360
 tggggagggg acggcttcta tgctatggac tactggggtc aaggaaccct ggtcaccgtc 420
 tcctcggcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
 gtgtcttggg actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtga caagaaagt 720
 ggtgagaggc cagcacaggg agggaggggtg tctgctggaa gcaggctcag cgctcctgcc 780
 tggacgcac cgggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
 ttcacccgga gcctctgccc gccccactca tgctcagggg gaggggtctt tggctttttc 900
 ccaggctctg ggcaggcaca ggctaggtgc ccctaaccga ggcctgcac acaaaggggc 960
 aggtgctggg ctacagacct ccaagagcca tatccgggag gaccctgccc ctgacctaac 1020
 cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat 1080

```

tccagtaact cccaatcttc tctctgcaga gcccaaactct tgtgacaaaa ctcacacatg 1140
cccaccgtgc ccaggtgaagc cagcccaggc ctcgccctcc agctcaaggc gggacagggtg 1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
tctcttcctc agcacctgaa ctccctggggg gaccgtcagt ctctctcttc ccccaaaaac 1320
ccaaggacac cctcatgac tcccggaccc ctgagggtcac atgcgtgggtg gtggacgtga 1380
gccacgaaga ccctgagggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaagacaaa gccgcggggag gagcagtaca acagcacgta ccgggtgggtc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag 1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtgggggtgc 1620
gagggccaca tggacagagg ccgggtcggc ccaccctctg ccctgagagt gaccgctgta 1680
ccaacctctg tcctacaggg cagccccgag aaccacagggt gtacaccctg ccccatccc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgagggt ctgcacaacc 1980
actacacgca gaagagcctc tcctgtctc cgggtaaata a 2021

```

<210> 54

<211> 472

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 54

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser

1	5	10	15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly			
20	25	30	
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly			
35	40	45	
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly			
50	55	60	
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr			
65	70	75	80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr			
85	90	95	
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp			
100	105	110	
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala			
115	120	125	
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser			
130	135	140	
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr			
145	150	155	160
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro			
165	170	175	
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val			
180	185	190	
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser			
195	200	205	
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile			
210	215	220	
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val			
225	230	235	240

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 245 250 255
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 260 265 270
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 275 280 285
 Val Asp Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 290 295 300
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 305 310 315 320
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 325 330 335
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 340 345 350
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 355 360 365
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 370 375 380
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 385 390 395 400
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 405 410 415
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 420 425 430
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 435 440 445
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 450 455 460
 Ser Leu Ser Leu Ser Pro Gly Lys
 465 470

<210> 55
 <211> 711
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 55
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 agaggagaca tccagatgac ccagtcctccg agctccctgt ccgcctctgt gggcgatagg 120
 gttaccatca cctgccgtgc cagtcaggat gtgaatactg ctgtagcctg gtatcaacag 180
 aaaccaggaa aagctccgaa actactgatt tactcggcatt ccttcctcta ctctggagtc 240
 ccttctcgct tctctggctc cagatctggg acggatttca ctctgacct cagcagtcgt 300
 cagccggaag acttcgcaac ttattactgt cagcaacatt atactactcc tcccagttc 360
 ggacagggtg ccaaggtgga gatcaaactg actgtggctg caccatctgt cttcatcttc 420
 ccgcatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
 ttctatccca gagaggccaa agtacagtggt aagggtggata acgccctcca atcggtgaac 540
 tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600
 ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
 cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgtta g 711

<210> 56
 <211> 236
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 56

```
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1           5           10           15
Val Ile Ile Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 20           25           30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 35           40           45
Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50           55           60
Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val
 65           70           75           80
Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr
 85           90           95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
100           105           110
His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
115           120           125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130           135           140
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145           150           155           160
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
165           170           175
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180           185           190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
195           200           205
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
210           215           220
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225           230           235
```

<210> 57

<211> 2489

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 57

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cgtttgtcct gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt 180
caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact 240
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gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga 360
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tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
```

```

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cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagt 720
ggtagagagg cagcacaggg agggaggggtg tctgctggaa gcaggctcag cgctcctgcc 780
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ttcaccggga gcctctgccc gccccactca tgctcagggg gagggctctc tggctttttc 900
ccaggctctg ggcaggcaca ggctaggtgc ccctaacca ggccctgcac acaaaggggc 960
aggtgctggg ctacagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaa 1020
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tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg 1140
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gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta 1680
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cctccgagca gctggtggcg ctgaagccct ggatcactcg ccagaacttc tcccggtgcc 2400
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tggaagccac agccccgaca gccccgtga 2489

```

<210> 58

<211> 628

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 58

```

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1           5           10           15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
20           25           30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35           40           45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
50           55           60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
65           70           75           80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
85           90           95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
100          105          110

```

Thr	Ala	Val	Tyr	Tyr	Cys	Ser	Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tyr	Ala		
		115					120					125					
Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser		
	130					135						140					
Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr		
145					150					155					160		
Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro		
				165					170					175			
Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val		
			180					185					190				
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser		
		195					200					205					
Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile		
	210					215					220						
Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val		
225					230					235					240		
Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala		
				245					250					255			
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro		
			260					265					270				
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val		
		275					280					285					
Val	Asp	Val	Ser	His	Glu	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp		
	290					295					300						
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln		
305					310					315					320		
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln		
				325					330					335			
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala		
		340						345					350				
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro		
		355					360					365					
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr		
	370					375					380						
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser		
385					390					395					400		
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr		
			405						410					415			
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr		
			420					425					430				
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe		
	435						440					445					
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys		
	450					455					460						
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His		
465					470					475					480		
Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp		
				485					490					495			
Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp		
			500					505					510				
Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp		
		515					520					525					
Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu		
	530					535					540						
Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln		
545					550					555					560		


```

ccgtggcctc caacctgcag gacgaggagc tctgcggggg cctctggcgg ctggtcctgg 2220
cacagcgctg gatggagcgg ctcaagactg tgcgtgggtc caagatgcaa ggcttgctgg 2280
agcgcgtaga cacggagata cactttgtca ccaaattgtc ctttcagccc cccccagct 2340
gtcttcgctt cgtccagacc aacatctccc gcctcctgca ggagacctcc gagcagctgg 2400
tggcgctgaa gccctggatc actcgccaga acttctcccc gtgcctggag ctgcagtgtc 2460
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cgacagcccc gtga 2534

```

<210> 60

<211> 643

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 60

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1           5           10           15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
          20           25           30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
          35           40           45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
          50           55           60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
65          70          75          80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
          85          90          95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
          100         105         110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
          115         120         125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
          130         135         140
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
145         150         155         160
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
          165         170         175
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
          180         185         190
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
          195         200         205
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
210         215         220
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
225         230         235         240
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
          245         250         255
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
          260         265         270
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
          275         280         285
Val Asp Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
          290         295         300
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305         310         315         320

```

Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	
				325					330					335		
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	
			340					345					350			
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	
		355					360					365				
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	
	370					375					380					
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	
385					390					395					400	
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	
			405						410					415		
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	
			420					425					430			
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	
	435						440					445				
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	
	450					455					460					
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
465					470				475						480	
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	
			485						490					495		
Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	
			500					505					510			
Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	
	515						520					525				
Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	
	530					535					540					
Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	
545					550					555					560	
Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	
			565						570					575		
Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	
			580					585					590			
Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	
		595					600					605				
Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	
	610					615					620					
Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala	Thr	Ala	Pro	
625					630					635					640	
Thr	Ala	Pro														

<210> 61

<211> 1998

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 61

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ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattacc agtcaccgtg 180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag 240

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cgcttcgtcc agaccaacat ctcccgcttc ctgcaggaga cctccgagca gctgggtggcg 420
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gccccggagc ccaaactcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 600
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tccccggacc ctgaggtcac atgctgggtg gtggacgtga gccacgaaga cctgaggtc 720
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ggctccagat ctgggacgga ttctactctg accatcagca gtctgcagcc ggaagacttc 1920
gcaacttatt actgtcagca acattatact actcctccca cgttcggaca gggtagcaag 1980
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```

<210> 62

<211> 665

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 62

```

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1           5           10           15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
 20           25           30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
 35           40           45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50           55           60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 65           70           75           80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 85           90           95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 100          105          110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 115          120          125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp

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130						135						140					
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro		
145						150					155				160		
Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala		
				165					170					175			
Thr	Ala	Pro	Thr	Ala	Pro	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr		
			180					185					190				
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe		
		195					200					205					
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro		
	210					215					220						
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val		
225				230						235					240		
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr		
			245					250						255			
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val		
			260					265					270				
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys		
		275					280					285					
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser		
	290					295					300						
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro		
305				310						315					320		
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val		
			325					330					335				
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly		
		340						345					350				
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp			
		355					360				365						
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp		
	370					375				380							
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His		
385				390						395					400		
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	Glu	Val		
			405					410					415				
Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu		
		420						425					430				
Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr	Tyr	Ile		
	435						440					445					
His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Arg		
450						455					460						
Ile	Tyr	Pro	Thr	Asn	Gly	Tyr	Thr	Arg	Tyr	Ala	Asp	Ser	Val	Lys	Gly		
465				470					475					480			
Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	Gln		
			485					490					495				
Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ser	Arg		
		500						505				510					
Trp	Gly	Gly	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr		
		515					520					525					
Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Gly	Gly		
	530					535					540						
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln		
545				550					555					560			
Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val		
			565					570					575				
Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Val	Asn	Thr	Ala	Val	Ala	Trp		

			580						585						590			
Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ser	Ala			
		595					600					605						
Ser	Phe	Leu	Tyr	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Arg	Ser			
	610					615					620							
Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe			
625					630					635					640			
Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	His	Tyr	Thr	Thr	Pro	Pro	Thr	Phe	Gly			
				645					650					655				
Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg										
		660					665											

<210> 63
 <211> 1098
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 63

atgacagtgc	tggcgccagc	ctggagccca	acaacctatc	tcctcctgct	gctgctgctg	60
agctcgggac	tcagtgggac	ccaggactgc	tccttccaac	acagcccat	ctcctccgac	120
ttcgctgtca	aatccgtga	gctgtctgac	tacctgcttc	aagattaccc	agtcaccgtg	180
gcctccaacc	tgcaggacga	ggagctctgc	gggggcctct	ggcggtggt	cctggcacag	240
cgctggatgg	agcggctcaa	gactgtcgct	gggtccaaga	tgcaaggctt	gctggagcgc	300
gtgaacacgg	agatacactt	tgtcaccaaa	tgtgcctttc	agccccccc	cagctgtctt	360
cgcttcgtcc	agaccaacat	ctccgcctc	ctgcaggaga	cctccgagca	gctggtggcg	420
ctgaagccct	ggatcaactc	ccagaacttc	tcccggtgcc	tggagctgca	gtgtcagccc	480
gactcctcaa	ccctgccacc	cccatggagt	ccccggcccc	tggaggccac	agccccgaca	540
gccccgggcg	gtggaggctc	tgggtggaggc	ggttcaggag	gcggtggatc	tgtgagagaa	600
agaggctctc	agagagtagc	agctcacata	actgggacca	gaggaagaag	caacacattg	660
tccttccaac	actccaagaa	tgaagaggct	ctggggccgca	aaataaaactc	ctgggaatca	720
tcaaggagtg	ggcattcatt	cctgagcaac	ttgcacttga	ggaatggtga	actggtcatc	780
catgaaaaag	ggttttacta	catctattcc	caaacatact	ttcgatttca	ggaggaaata	840
aaagaaaaca	caaagaacga	caaacaaatg	gtccaatata	tttacaata	cacaagttat	900
cctgacccta	tattgttgat	gaaaagtgc	agaaatagtt	gttggtctaa	agatgcagaa	960
tatggactct	attccatcta	tcaaggggga	atatttgagc	ttaaggaaaa	tgacagaatt	1020
tttgtttctg	taacaaatga	gcacttgata	gacatggacc	atgaagccag	tttttttggg	1080
gccttttttag	ttggctaa					1098

<210> 64
 <211> 365
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 64

Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Thr	Thr	Tyr	Leu	Leu	Leu
1				5				10					15		
Leu	Leu	Leu	Leu	Ser	Ser	Gly	Leu	Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe
			20				25					30			
Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu
	35						40					45			

Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu
50						55					60				
Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
65					70					75					80
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
				85					90					95	
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
			100					105					110		
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
		115					120					125			
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
						135						140			
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
145					150					155					160
Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala
				165					170					175	
Thr	Ala	Pro	Thr	Ala	Pro	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
			180					185					190		
Gly	Gly	Gly	Gly	Ser	Val	Arg	Glu	Arg	Gly	Pro	Gln	Arg	Val	Ala	Ala
		195					200					205			
His	Ile	Thr	Gly	Thr	Arg	Gly	Arg	Ser	Asn	Thr	Leu	Ser	Ser	Pro	Asn
	210					215					220				
Ser	Lys	Asn	Glu	Lys	Ala	Leu	Gly	Arg	Lys	Ile	Asn	Ser	Trp	Glu	Ser
225					230					235					240
Ser	Arg	Ser	Gly	His	Ser	Phe	Leu	Ser	Asn	Leu	His	Leu	Arg	Asn	Gly
				245					250					255	
Glu	Leu	Val	Ile	His	Glu	Lys	Gly	Phe	Tyr	Tyr	Ile	Tyr	Ser	Gln	Thr
		260						265					270		
Tyr	Phe	Arg	Phe	Gln	Glu	Glu	Ile	Lys	Glu	Asn	Thr	Lys	Asn	Asp	Lys
		275					280					285			
Gln	Met	Val	Gln	Tyr	Ile	Tyr	Lys	Tyr	Thr	Ser	Tyr	Pro	Asp	Pro	Ile
	290					295						300			
Leu	Leu	Met	Lys	Ser	Ala	Arg	Asn	Ser	Cys	Trp	Ser	Lys	Asp	Ala	Glu
305					310					315					320
Tyr	Gly	Leu	Tyr	Ser	Ile	Tyr	Gln	Gly	Gly	Ile	Phe	Glu	Leu	Lys	Glu
				325					330					335	
Asn	Asp	Arg	Ile	Phe	Val	Ser	Val	Thr	Asn	Glu	His	Leu	Ile	Asp	Met
			340					345					350		
Asp	His	Glu	Ala	Ser	Phe	Phe	Gly	Ala	Phe	Leu	Val	Gly			
	355						360					365			

<210> 65

<211> 1203

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 65

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agctcggggac tcagtgggac ccaggactgc tcttccaac acagcccat ctcctccgac 120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggtggt cctggcacag 240
cgctggatgg agcggctcaa gactgtcgct gggccaaga tgcaaggctt gctggagcgc 300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agccccccc cagctgtctt 360

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cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg 420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
gactcctcaa ccctgccacc cccatggagt ccccgccccc tggaggccac agccccgaca 540
gccccgatga agcagatcga ggacaaaatt gaggaatcc tgtccaagat ttaccacatc 600
gagaacgaga tcgcccggat taagaaactc attggcgaga cctctgagga aaccatttct 660
acagttcaag aaaagcaaca aaatatttct cccctagtga gagaaagagg tcctcagaga 720
gtagcagctc acataactgg gaccagagga agaagcaaca cattgtcttc tccaaactcc 780
aagaatgaaa aggctctggg ccgcaaaata aactcctggg aatcatcaag gagtgggcat 840
tcattcctga gcaacttgca cttgaggaat ggtgaactgg tcatccatga aaaagggttt 900
tactacatct attcccaaac atactttcga tttcaggagg aaataaaaga aaacacaaag 960
aacgacaaac aaatggtcca atatatttac aaatacacaa gttatcctga ccctatattg 1020
ttgatgaaaa gtgctagaaa tagttgttgg tctaaagatg cagaatatgg actctattcc 1080
atctatcaag ggggaatatt tgagcttaag gaaaatgaca gaatttttgt ttctgtaaca 1140
aatgagcact tgatagacat ggaccatgaa gccagttttt ttggggcctt tttagttggc 1200
taa 1203

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<210> 66

<211> 400

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 66

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Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1          5          10          15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
20          25          30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
35          40          45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50          55          60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65          70          75          80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
85          90          95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
100         105         110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
115         120         125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
130         135         140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145         150         155         160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
165         170         175
Thr Ala Pro Thr Ala Pro Met Lys Gln Ile Glu Asp Lys Ile Glu Glu
180         185         190
Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys
195         200         205
Lys Leu Ile Gly Glu Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu
210         215         220
Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg
225         230         235         240
Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
245         250         255

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Ser	Pro	Asn	Ser	Lys	Asn	Glu	Lys	Ala	Leu	Gly	Arg	Lys	Ile	Asn	Ser
		260						265					270		
Trp	Glu	Ser	Ser	Arg	Ser	Gly	His	Ser	Phe	Leu	Ser	Asn	Leu	His	Leu
		275					280					285			
Arg	Asn	Gly	Glu	Leu	Val	Ile	His	Glu	Lys	Gly	Phe	Tyr	Tyr	Ile	Tyr
	290					295					300				
Ser	Gln	Thr	Tyr	Phe	Arg	Phe	Gln	Glu	Glu	Ile	Lys	Glu	Asn	Thr	Lys
305					310					315					320
Asn	Asp	Lys	Gln	Met	Val	Gln	Tyr	Ile	Tyr	Lys	Tyr	Thr	Ser	Tyr	Pro
			325						330					335	
Asp	Pro	Ile	Leu	Met	Lys	Ser	Ala	Arg	Asn	Ser	Cys	Trp	Ser	Lys	
		340					345					350			
Asp	Ala	Glu	Tyr	Gly	Leu	Tyr	Ser	Ile	Tyr	Gln	Gly	Gly	Ile	Phe	Glu
	355						360				365				
Leu	Lys	Glu	Asn	Asp	Arg	Ile	Phe	Val	Ser	Val	Thr	Asn	Glu	His	Leu
	370					375					380				
Ile	Asp	Met	Asp	His	Glu	Ala	Ser	Phe	Phe	Gly	Ala	Phe	Leu	Val	Gly
385					390					395					400

<210> 67

<211> 1749

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 67

atgacagtgc	tggcgccagc	ctggagccca	acaacctatc	tcctcctgct	gctgctgctg	60
agctcgggac	tcagtgggac	ccaggactgc	tccttccaac	acagcccat	ctcctccgac	120
ttcgtgtgca	aaatccgtga	gctgtctgac	tacctgcttc	aagattacc	agtcaccgtg	180
gcctccaacc	tgcaggacga	ggagctctgc	gggggcctct	ggcggtggt	cctggcacag	240
cgctggatgg	agcggctcaa	gactgtcgct	gggtccaaga	tgcaaggctt	gctggagcgc	300
gtgaacacgg	agatacactt	tgtcaccaaa	tgtgcctttc	agccccccc	cagctgtctt	360
cgttcgtcc	agaccaacat	ctcccgctc	ctgcaggaga	cctccgagca	gctgggtggc	420
ctgaagccct	ggatcactcg	ccagaacttc	tcccggtgcc	tggagctgca	gtgtcagccc	480
gactcctcaa	ccctgccacc	cccatggagt	ccccggcccc	tggaggccac	agccccgaca	540
gccccggagc	ccaaatcttg	tgacaaaact	cacacatgcc	caccgtgccc	agcacctgaa	600
ctcctggggg	gaccgtcagt	cttcctcttc	cccccaaaac	ccaaggacac	cctcatgata	660
tcccggaccc	ctgagggtcac	atgcgtgggt	gtggacgtga	gccacgaaga	ccctgagggt	720
aagttcaact	ggtacgtgga	cggcgtggag	gtgcataatg	ccaagacaaa	gccgcggggg	780
gagcagtaca	acagcacgta	ccgggtgggt	tgcgtcctca	ccgtcctgca	ccaggactgg	840
ctgaatggca	aggagtacaa	gtgcaagggt	tccaacaaag	ccctcccagc	ccccatcgag	900
aaaaccatct	ccaaagccaa	agggcagccc	cgagaaccac	aggtgtacac	cctgccccca	960
tcccgggatg	agctgaccaa	gaaccagggt	agcctgacct	gcctgggtcaa	aggcttctat	1020
cccagcgaca	tcgccgtgga	gtgggagagc	aatgggcagc	cggagaacaa	ctacaagacc	1080
acgcctcccg	tgttggaact	cgacggctcc	ttcttcctct	acagcaagct	caccgtggac	1140
aagagcaggt	ggcagcaggg	gaacgtcttc	tcattgctcc	tgatgcatga	ggctctgcac	1200
aaccactaca	cgcagaagag	cctctccctg	tctcccggtg	aagtgaagag	aagaggctct	1260
cagagagtag	cagctcacat	aactgggacc	agaggaagaa	gcaacacatt	gtcttctcca	1320
aactccaaga	atgaaaaggc	tctgggccc	aaaataaact	cctgggaatc	atcaaggagt	1380
gggcattcat	tcctgagcaa	cttgcaactg	aggaatgggt	aactgggtcat	ccatgaaaaa	1440
gggttttact	acatctattc	ccaaacatac	tttcgatttc	aggaggaaat	aaaagaaaac	1500
acaaagaacg	acaaacaaat	ggtccaatat	atttacaat	acacaagtta	tcctgaccct	1560
atattgttga	tgaaaagtgc	tagaaatagt	tgttggtcta	aagatgcaga	atatggactc	1620

tattccatct atcaaggggg aatatttgag ctttaaggaaa atgacagaat ttttgtttct 1680
 gtaacaaatg agcacttgat agacatggac catgaagcca gtttttttgg ggccttttta 1740
 gttggctaa 1749

<210> 68
 <211> 582
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 68
 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1 5 10 15
 Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
 20 25 30
 Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
 35 40 45
 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50 55 60
 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 65 70 75 80
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 85 90 95
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 100 105 110
 Phe Gln Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 115 120 125
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
 130 135 140
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
 145 150 155 160
 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
 165 170 175
 Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 180 185 190
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 195 200 205
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 210 215 220
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 225 230 235 240
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 245 250 255
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 260 265 270
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 275 280 285
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 290 295 300
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 305 310 315 320
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 325 330 335
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 340 345 350

Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	
		355					360					365				
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	
	370					375					380					
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	
385					390					395					400	
Asn	His	Tyr	Thr		Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	Val	Arg
				405						410					415	
Glu	Arg	Gly	Pro	Gln	Arg	Val	Ala	Ala	His	Ile	Thr	Gly	Thr	Arg	Gly	
			420						425					430		
Arg	Ser	Asn	Thr	Leu	Ser	Ser	Pro	Asn	Ser	Lys	Asn	Glu	Lys	Ala	Leu	
		435					440					445				
Gly	Arg	Lys	Ile	Asn	Ser	Trp	Glu	Ser	Ser	Arg	Ser	Gly	His	Ser	Phe	
	450					455					460					
Leu	Ser	Asn	Leu	His	Leu	Arg	Asn	Gly	Glu	Leu	Val	Ile	His	Glu	Lys	
465					470					475					480	
Gly	Phe	Tyr	Tyr	Ile	Tyr	Ser	Gln	Thr	Tyr	Phe	Arg	Phe	Gln	Glu	Glu	
				485					490					495		
Ile	Lys	Glu	Asn	Thr	Lys	Asn	Asp	Lys	Gln	Met	Val	Gln	Tyr	Ile	Tyr	
			500					505					510			
Lys	Tyr	Thr	Ser	Tyr	Pro	Asp	Pro	Ile	Leu	Leu	Met	Lys	Ser	Ala	Arg	
		515					520					525				
Asn	Ser	Cys	Trp	Ser	Lys	Asp	Ala	Glu	Tyr	Gly	Leu	Tyr	Ser	Ile	Tyr	
	530					535					540					
Gln	Gly	Gly	Ile	Phe	Glu	Leu	Lys	Glu	Asn	Asp	Arg	Ile	Phe	Val	Ser	
545					550					555					560	
Val	Thr	Asn	Glu	His	Leu	Ile	Asp	Met	Asp	His	Glu	Ala	Ser	Phe	Phe	
				565					570					575		
Gly	Ala	Phe	Leu	Val	Gly											
			580													